



#7

Carp0089.ST25.txt

## SEQUENCE LISTING

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Sub- <120> Biological Products

DI- <130> Carp-0089

<140> 09/875,221

<141> 2001-06-06

<150> GB0013810.7

<151> 2000-06-06

<160> 130

<170> PatentIn version 3.1

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 gac cgg gtc acc atc act tgt aaa gcc agt cag aac gta ggt act aac 96  
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn  
 20 25 30  
 gta gcc tgg tat cag caa aaa cca ggt aaa gcc cca aaa gcc ctc atc 144  
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile  
 35 40 45  
 tac agt gcc tct ttc ctc tat agt ggt gta cca tac agg ttc agc gga 192  
 Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly  
 50 55 60  
 tcc ggt agt ggt act gat ttc acc ctc acg atc agt agc ctc cag cca 240  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 gaa gat ttc gcc act tat tac tgt caa cag tat aac atc tac cca ctc 288  
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu  
 85 90 95  
 aca ttc ggt cag ggt act aaa gta gaa atc aaa 321  
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 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn  
 20 25 30  
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile  
 35 40 45

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Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly  
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu  
 85 90 95

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 gac cgg gtc acc atc act tgt aaa gcc agt cag aac gta ggt act aac 96  
 Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn  
 20 25 30  
 gta gcc tgg tat cag caa aaa cca ggt aaa gcc cca aaa ctc ctc atc 144  
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45  
 tac agt gcc tct ttc ctc tat agt ggt gta cca tac agg ttc agc gga 192  
 Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly  
 50 55 60  
 tcc ggt agt ggt act gat ttc acc ctc acg atc agt agc ctc cag cca 240  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 gaa gat ttc gcc act tat tac tgt caa cag tat aac atc tac cca ctc 288  
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu  
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Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15

tcc gtc aaa gtt tcg tgt aag gcc tca ggc tac gtg ttc aca gac tat 96  
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr  
20 25 30

ggt atg aat tgg gtc aga cag gcc ccg gga caa ggc ctg gaa tgg atg 144  
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45

ggt tgg att aat act tac att gga gag cct att tat gct caa aag ttc 192  
Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Gln Lys Phe  
50 55 60

cag ggc aga gtc acg ttc act cta gac acc tcc aca agc act gca tac 240

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Gln Gly Arg Val Thr Phe Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr  
65 70 75 80

atg gag ctg tca tct ctg aga tcc gag gac acc gca gtg tac tat tgt 288  
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

gct aga gga tac aga tct tat gcc atg gac tac tgg ggc cag ggt acc 336  
Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr  
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cta gtc aca gtc tcc tca 354  
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20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Gln Lys Phe  
50 55 60

Gln Gly Arg Val Thr Phe Thr Leu Asp Thr Ser Thr Ser Thr Ala Tyr  
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
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 tca ctg aga ttg tcc tgt gct gca tct ggt tac gtc ttc aca gac tat 96  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Val Phe Thr Asp Tyr  
 20 25 30  
 gga atg aat tgg gtt aga cag gcc ccg gga aag ggc ctg gaa tgg atg 144  
 Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45  
 ggt tgg att aat act tac att gga gag cct att tat gct gac agc gtc 192  
 Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val  
 50 55 60  
 aag ggc aga ttc acg ttc tct cta gac aca tcc aag tca aca gca tac 240  
 Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr  
 65 70 75 80  
 ctc caa atg aat agc ctg aga gca gag gac acc gca gtg tac tat tgt 288  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 gct aga gga tac aga tct tat gcc atg gac tac tgg ggc cag ggt acc 336  
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 35 40 45  
 Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr  
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21

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gctgacagac taacagactg ttcc 24

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talcagcaaa 70

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 ccaggctacg t 71

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<210> 62  
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&lt;212&gt; DNA

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&lt;223&gt; Primer P7990

&lt;400&gt; 68

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71

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71

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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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&lt;223&gt; Primer P7995

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&lt;211&gt; 56

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Primer P7992

&lt;400&gt; 71

ccatgtatgc agtgcgttgt ggaggtgtct agagtgaacg tgaatctgcc cttgaa

56

&lt;210&gt; 72

&lt;211&gt; 62

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Primer P7993

<400> 72  
ccacaagcac tgcatacatg gagctgtcat ctctgagatc cgaggacacc gcagtgtact 60  
at 62

<210> 73  
<211> 78  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer P7994

<400> 73  
gaattcggta ccctggcccc agtagtccat ggcataagat ctgtatcctc tagcacaata 60  
gtacactgcg gtgtcctc 78

<210> 74  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer 7988

<400> 74  
gaattcgtgc actctcaggt gcagctggtc 30

<210> 75  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer P7987

<400> 75  
gaattcggta ccctggcccc agtagtccat 30

<210> 76  
<211> 65  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer P7999

<400> 76  
gatccgccag gctgcacgag accgcctcct gactcgacca gctgaacctc agagtgcacg 60  
aattc 65

<210> 77  
<211> 71  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Primer P8000

<400> 77  
 tctcgtgcag cctggcggat cgctgagatt gtcctgtgct gcatctgggtt acgtcttcac 60  
 agactatgga a 71

<210> 78

<211> 71

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer P8001

<400> 78  
 ccaacccatc catttcaggc cctttcccg ggccctgctta acccaattca ttccatagtc 60  
 tgtgaagacg t 71

<210> 79

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer P7997

<400> 79  
 ggaggtatgc tgttgacttg gatgtgtcta gagagaacgt gaatctgccc ttgaa 55

<210> 80

<211> 62

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer P7998

<400> 80  
 ccaagtcaac agcatacctc caaatgaata gcctgagagc agaggacacc gcagtgtact 60  
 at 62

<210> 81

<211> 78

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer P7993

<400> 81  
 gaattcggta ccctggcccc agtagtccat ggcataagat ctgtatcctc tagcacaata 60  
 gtacactgcg gtgtcctc 78

<210> 82

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer P7996

<400> 82

gaattcgtgc actctgaggt tcagctggtc

30

<210> 83

<211> 74

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' Primer

<400> 83

cgcgcgcaa ttgcagtggc cttggctggt ttcgctaccg tagcgcaagc tgacattcaa

60

atgacccaga gccc

74

<210> 84

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' Primer

<400> 84

ttcaactgct catcagatgg

20

<210> 85

<211> 78

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' Primer

<400> 85

gctatcgcaa ttgcagtggc gctagctggt ttcgccaccg tggcgcaagc tgaggttcag

60

ctggtcgagt caggaggc

78

<210> 86

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' Primer

<400> 86

gcctgagttc cacgacac

18

<210> 87

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Human Group 1 consensus framework L1

<400> 87

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys  
20

<210> 88

<211> 69

<212> PRT

<213> Artificial Sequence

<220>

<223> hTNF40 framework L1

<400> 88

Ala Ser Pro Ile Leu Glu Val Ala Leu Met Glu Thr Thr His Arg Gly  
1 5 10 15

Leu Asn Ser Glu Arg Gly Leu Asn Leu Tyr Ser Pro His Glu Met Glu  
20 25 30

Thr Ser Glu Arg Thr His Arg Ser Glu Arg Val Ala Leu Gly Leu Tyr  
35 40 45

Ala Ser Pro Ala Arg Gly Val Ala Leu Ser Glu Arg Val Ala Leu Thr  
50 55 60

His Arg Cys Tyr Ser  
65

<210> 89

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Human group 1 consensus framework L2

<400> 89

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr  
1 5 10 15

<210> 90

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> hTNF40 framework L2

&lt;400&gt; 90

Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Ala	Leu	Ile	Tyr
1				5					10					15

&lt;210&gt; 91

&lt;211&gt; 32

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human group 1 consensus framework L3

&lt;400&gt; 91

Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr
1				5					10					15	

Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys
			20					25					30		

&lt;210&gt; 92

&lt;211&gt; 32

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; hTNF40 framework L3

&lt;400&gt; 92

Gly	Val	Pro	Tyr	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr
1				5					10					15	

Leu	Thr	Ile	Ser	Thr	Val	Gln	Ser	Glu	Asp	Leu	Ala	Glu	Tyr	Phe	Cys
			20					25					30		

&lt;210&gt; 93

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human group 1 consensus framework L4

&lt;400&gt; 93

Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg
1				5					10	

&lt;210&gt; 94

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; hTNF40 framework L4

&lt;400&gt; 94

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg  
1 5 10

&lt;210&gt; 95

&lt;211&gt; 30

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human group 1 consensus framework H1

&lt;400&gt; 95

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala  
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr  
20 25 30

&lt;210&gt; 96

&lt;211&gt; 30

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; hTNF40 framework H1

&lt;400&gt; 96

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu  
1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr  
20 25 30

&lt;210&gt; 97

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human group 1 consensus framework H2

&lt;400&gt; 97

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly  
1 5 10

&lt;210&gt; 98

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; hTNF40 framework H2

&lt;400&gt; 98



Trp Val Lys Gln Ala Pro Gly Lys Ala Phe Lys Trp Met Gly  
1 5 10

<210> 99  
<211> 32  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Human group 1 consensus framework H3

<400> 99

Arg Val Thr Ile Thr Arg Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu  
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg  
20 25 30

<210> 100  
<211> 32  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> hTNF40 framework H3

<400> 100

Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe Leu Gln  
1 5 10 15

Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys Ala Arg  
20 25 30

<210> 101  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Human group 1 consensus framework H4

<400> 101

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
1 5 10

<210> 102  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> hTNF40 framework H4

<400> 102

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser  
1 5 10

<210> 103  
<211> 324  
<212> DNA  
<213> Murine

<220>  
<221> CDS  
<222> (1)..(324)  
<223>

<400> 103  
gac att gtg atg acc cag tct caa aaa ttc atg tcc aca tca gta gga 48  
Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly  
1 5 10 15  
  
gac agg gtc agc gtc acc tgc aag gcc agt cag aat gtg ggt act aat 96  
Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn  
20 25 30  
  
gta gcc tgg tat caa cag aaa cca gga caa tct cct aaa gca ctg att 144  
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile  
35 40 45  
  
tac tcg gca tcc ttc cta tat agt gga gtc cct tat cgc ttc aca ggc 192  
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Thr Gly  
50 55 60  
  
agt gga tct ggg aca gat ttc act ctc acc atc agc act gtg cag tct 240  
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Val Gln Ser  
65 70 75 80  
  
gaa gac ttg gca gag tat ttc tgt cag caa tat aac atc tat cct ctc 288  
Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ile Tyr Pro Leu  
85 90 95  
  
acg ttc ggt gct ggg acc aag ctg gag ctg aaa cgt 324  
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg  
100 105

<210> 104  
<211> 108  
<212> PRT  
<213> Murine

<400> 104

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly  
1 5 10 15  
  
Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn  
20 25 30  
  
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile  
35 40 45  
  
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Thr Gly

50

55

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Val Gln Ser  
65 70 75 80

Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ile Tyr Pro Leu  
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg  
100 105

<210> 105  
<211> 354  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> hTNF40 heavy chain variable domain

<220>  
<221> CDS  
<222> (1)..(354)  
<223>

<400> 105  
cag atc cag ttg gtg cag tct gga cct gag ctg aag aag cct gga gag 48  
Gln-Ile Gln Leu-Val Gln-Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu  
1 5 10 15  
aca gtc aag atc tcc tgc aag gct tct gga tat gtt ttc aca gac tat 96  
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr  
20 25 30  
gga atg aat tgg gtg aag cag gct cca gga aag gct ttc aag tgg atg 144  
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Ala Phe Lys Trp Met  
35 40 45  
ggc tgg ata aac acc tac att gga gag cca ata tat gtt gat gac ttc 192  
Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Val Asp Asp Phe  
50 55 60  
aag gga cga ttt gcc ttc tct ttg gaa acc tct gcc agc act gcc ttt 240  
Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe  
65 70 75 80  
ttg cag atc aac aac ctc aaa aat gag gac acg gct aca tat ttc tgt 288  
Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys  
85 90 95  
gca aga ggt tac cgg tcc tat gct atg gac tac tgg ggt caa gga acc 336  
Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr  
100 105 110  
tca gtc acc gtc tct tca 354  
Ser Val Thr Val Ser Ser  
115

<210> 106  
<211> 118

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; hTNF40 heavy chain variable domain

&lt;400&gt; 106

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu  
 1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr  
 20 25 30

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Ala Phe Lys Trp Met  
 35 40 45

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Val Asp Asp Phe  
 50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe  
 65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys  
 85 90 95

Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr  
 100 105 110

Ser Val Thr Val Ser Ser  
 115

&lt;210&gt; 107

&lt;211&gt; 84

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; OmpA oligonucleotide adaptor

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (29)..(67)

&lt;223&gt;

&lt;400&gt; 107

tcgagttcta gataacgagg cgtaaaaa atg aaa aag aca gct atc gca att 52  
 Met Lys Lys Thr Ala Ile Ala Ile  
 1 5

gca gtg gcc ttg gct ctgacgtacg agtcagg 84  
 Ala Val Ala Leu Ala  
 10

&lt;210&gt; 108

<211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> OmpA oligonucleotide adaptor

<400> 108

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala  
 1 5 10

<210> 109  
 <211> 67  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IGS cassette-1

<220>  
 <221> CDS  
 <222> (2)..(40)  
 <223>

<220>  
 <221> CDS  
 <222> (43)..(66)  
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<400> 109  
 g agc tca cca gta aca aaa agt ttt aat aga gga gag tgt ta atg aag 48  
 Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Met Lys  
 1 5 10 15

aag act gct ata gca att g 67  
 Lys Thr Ala Ile Ala Ile  
 20

<210> 110  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IGS cassette-1

<400> 110

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 1 5 10

<210> 111  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IGS cassette-1

&lt;400&gt; 111

Met Lys Lys Thr Ala Ile Ala Ile  
 1 5

&lt;210&gt; 112

&lt;211&gt; 69

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; IGS cassette-2

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (2)..(43)

&lt;223&gt;

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (45)..(68)

&lt;223&gt;

&lt;400&gt; 112

g agc tca cca gta aca aaa agt ttt aat aga ggg gag tgt taa a atg 47  
 Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys Met  
 1 5 10

aag aag act gct ata gca att g 69  
 Lys Lys Thr Ala Ile Ala Ile  
 15 20

&lt;210&gt; 113

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; IGS cassette-2

&lt;400&gt; 113

Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 1 5 10

&lt;210&gt; 114

&lt;211&gt; 8

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; IGS cassette-2

&lt;400&gt; 114

Met Lys Lys Thr Ala Ile Ala Ile  
 1 5

&lt;210&gt; 115

<211> 81  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IGS cassette-3

<220>  
 <221> CDS  
 <222> (2)..(43)  
 <223>

<220>  
 <221> CDS  
 <222> (57)..(80)  
 <223>

<400> 115  
 g agc tca cca gta aca aaa agc ttt aat aga gga gag tgt tga 43  
 Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 1 5 10

ggaggaaaaa aaa atg aag aaa act ggt ata gca att g 81  
 Met Lys Lys Thr Ala Ile Ala Ile  
 15 20

<210> 116  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IGS cassette-3

<400> 116  
 Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 1 5 10

<210> 117  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IGS cassette-3

<400> 117  
 Met Lys Lys Thr Ala Ile Ala Ile  
 1 5

<210> 118  
 <211> 81  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> IGS cassette-4

<220>  
 <221> CDS  
 <222> (2)..(43)  
 <223>

<220>  
 <221> CDS  
 <222> (57)..(80)  
 <223>

<400> 118  
 g agc tca cca gta aca aaa agt ttt aat aga gga gag tgt tga 43  
 Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 1 5 10

cgaggattat ata atg aag aaa act gct ata gca att g 81  
 Met Lys Lys Thr Ala Ile Ala Ile  
 15 20

<210> 119  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IGS cassette-4

<400> 119  
 Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 1 5 10

<210> 120  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IGS cassette-4

<400> 120  
 Met Lys Lys Thr Ala Ile Ala Ile  
 1 5

<210> 121  
 <211> 30  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Human group 3 consensus framework H1

<400> 121  
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser



20

25

30

&lt;210&gt; 122

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human group 3 consensus framework H2

&lt;400&gt; 122

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser  
 1 5 10

&lt;210&gt; 123

&lt;211&gt; 32

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human group 3 consensus framework H3

&lt;400&gt; 123

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln  
 1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg  
 20 25 30

&lt;210&gt; 124

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Human group 3 consensus framework H4

&lt;400&gt; 124

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
 1 5 10

&lt;210&gt; 125

&lt;211&gt; 648

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Grafted heavy chain for fab

&lt;400&gt; 125

gaggttcagc tggctcagtc aggaggcggc ctcgtgcagc ctggcggatc actgagattg 60

tcctgtgctg catctgggta cgtcttcaca gactatggaa tgaattgggt tagacaggcc 120

ccgggaaagg gcctggaatg gatggggttgg attaatactt acattggaga gcctatttat 180

gctgacagcg tcaagggcag attcacgttc tctctagaca catccaagtc aacagcatac 240

Carp0089.ST25.txt

ctccaatga atagcctgag agcagaggac accgcagtgt actattgtgc tagaggatac 300  
 agatcttatg ccatggacta ctggggccag ggtaccctag tcacagtctc ctcagcttcc 360  
 accaagggcc catcggtctt cccctggca ccctctcca agagcacctc tgggggcaca 420  
 gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480  
 tcaggcgccc tgaccagcgg cgtgcacacc ttcccggtg tctacagtc ctcaggactc 540  
 tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 600  
 tgcaacgtga atcacaagcc cagcaacacc aaggtcgaca agaaagtt 648

<210> 126

<211> 216

<212> PRT

<213> Artificial Sequence

<220>

<223> Grafted heavy chain for fab

<400> 126

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Val Phe Thr Asp Tyr  
 - 20 - 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr  
 100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro  
 115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
 130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
 145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
 165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser  
 180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser  
 195 200 205

Asn Thr Lys Val Asp Lys Lys Val  
 210 215

<210> 127

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> Grafted light chain for fab and modified fab

<400> 127

gacattcaaa tgacccagag cccatccagc ctgagcgcat ctgtaggaga ccgggtcacc 60

atcacttgta aagccagtca gaacgtaggt actaacgtag cctggtatca gcaaaaacca 120

ggtaaagccc caaaagccct catctacagt gcctctttcc tctatagtgg tgtaccatac 180

aggttcagcg gatccggtag tgggtactgat ttcaccctca cgatcagtag cctccagcca 240

gaagatttcg ccacttatta ctgtcaacag tataacatct acccactcac attcggtcag 300

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cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

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<210> 128

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Grafted light chain for fab and modified fab

<400> 128

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
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Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn  
 20 25 30

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Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile  
35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 129

<211> 687

<212> DNA

<213> Artificial Sequence

<220>

<223> Grafted heavy chain for modified fab

<400> 129

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ccgggaaagg gcctggaatg gatgggttggt attaatactt acattggaga gcctatttat 180

gctgacagcg tcaagggcag attcacgttc tctctagaca catccaagtc aacagcatac 240  
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 accaagggcc catcggcttc cccctggca cctcctcca agagcacctc tgggggcaca 420  
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 tcaggcgccc tgaccagcgg cgtgcacacc ttcccgctg tcctacagtc ctcaggactc 540  
 tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacac 600  
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<210> 130  
 <211> 229  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Grafted heavy chain for modified fab

<400> 130

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Val Phe Thr Asp Tyr  
 20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met  
 35 40 45

Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr  
 100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro  
 115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
 130 135 140

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Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser  
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser  
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr  
210 215 220

His Thr Cys Ala Ala  
225